

## SEQUENCE LISTING

<110> Basi, Guriq  
Saldanha, Jose  
Yednock, Ted

<120> Humanized Antibodies that Recognize  
Beta-Amyloid Peptide

<130> ELN-002

<150> 60/251,892  
<151> 2000-12-06

<160> 63

<170> FastSEQ for Windows Version 4.0

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<220>  
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<222> (1)...(396)

<221> sig\_peptide  
<222> (1)...(60)

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-20	-15	-10	-5
gaa acc aac ggt tat gtt gtg atg acc cag act cca ctc act ttg tcg	96		
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser			
1	5	10	
gtt acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc	144		
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser			
15	20	25	
ctc tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg	192		
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg			
30	35	40	
cca ggc cag tct cca aag cgc cta atc tat ctg gtg tct aaa ctg gac	240		
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp			
45	50	55	60
tct gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttt	288		
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe			
65	70	75	

aca ctg aaa atc agc aga ata gag gct gag gat ttg gga ctt tat tat	336
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr	
80	85
	90
tgc tgg caa ggt aca cat ttt cct cgg acg ttc ggt gga ggc acc aag	384
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Thr Lys	
95	100
	105
ctg gaa atc aaa	396
Leu Glu Ile Lys	
110	

<210> 2  
 <211> 132  
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<220>  
 <221> SIGNAL  
 <222> (1)...(20)

<400> 2			
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-20	-15	-10	-5
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser			
1	5	10	
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser			
15	20	25	
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg			
30	35	40	
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp			
45	50	55	60
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe			
65	70	75	
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr			
80	85	90	
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Thr Lys			
95	100	105	
Leu Glu Ile Lys			
110			

<210> 3  
 <211> 414  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(414)

<221> sig\_peptide  
 <222> (1)...(57)

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     -15                  -10                  -5  
  
 gtc cag tgt gaa gtg aag ctg gtg gag tct ggg gga ggc tta gtg aag 96  
 Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Leu Val Lys  
     1                  5                  10  
  
 cct gga gcg tct ctg aaa ctc tcc tct gca gcc tct gga ttc act ttc 144  
 Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
     15                  20                  25  
  
 agt aac tat ggc atg tct tgg gtt cgc cag aat tca gac aag agg ctg 192  
 Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu  
     30                  35                  40                  45  
  
 gag tgg gtt gca tcc att agg agt ggt ggt aga acc tac tat tca 240  
 Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Arg Thr Tyr Tyr Ser  
     50                  55                  60  
  
 gac aat gta aag ggc cga ttc acc atc tcc aga gag aat gcc aag aac 288  
 Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn  
     65                  70                  75  
  
 acc ctg tac ctg caa atg agt agt ctg aag tct gag gac acg gcc ttg 336  
 Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu  
     80                  85                  90  
  
 tat tat tgt gtc aga tat gat cac tat agt ggt agc tcc gac tac tgg 384  
 Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp  
     95                  100                  105  
  
 ggc cag ggc acc act gtc aca gtc tcc tca 414  
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
     110                  115

<210> 4  
 <211> 138  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> SIGNAL  
 <222> (1)...(19)

<400> 4  
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 Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Leu Val Lys  
     1                  5                  10  
 Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
     15                  20                  25  
 Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu  
     30                  35                  40                  45

Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser  
50 55 60  
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn  
65 70 75  
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu  
80 85 90  
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp  
95 100 105  
Gly Gln Gly Thr Thr Ile Thr Val Ser Ser  
110 115

<210> 5  
<211> 132  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> SIGNAL  
<222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 5  
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg  
-20 -15 -10 -5  
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro  
1 5 10  
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser  
15 20 25  
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys  
30 35 40  
Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp  
45 50 55 60  
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe  
65 70 75  
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
80 85 90  
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys  
95 100 105  
Val Glu Ile Lys  
110

<210> 6  
<211> 125  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> (1)...(19)

<400> 6

Met Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val  
-15 -10 -5  
Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala  
1 5 10  
Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr  
15 20 25  
Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu  
30 35 40 45  
Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe  
50 55 60  
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val  
65 70 75  
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr  
80 85 90  
Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

<210> 7  
<211> 100  
<212> PRT  
<213> Homo sapiens

<400> 7  
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly  
1 5 10 15  
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
20 25 30  
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
35 40 45  
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro  
50 55 60  
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
65 70 75 80  
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala  
85 90 95  
Leu Gln Thr Pro  
100

<210> 8  
<211> 138  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Humanized 3D6 heavy chain variable region

<221> SIGNAL  
<222> (1)...(19)

<400> 8  
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly  
-15 -10 -5  
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln  
1 5 10

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 15 20 25  
 Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 30 35 40 45  
 Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Arg Thr Tyr Tyr Ser  
 50 55 60  
 Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
 65 70 75  
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu  
 80 85 90  
 Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp  
 95 100 105  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 110 115

<210> 9  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 9  
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30  
 Ala Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys  
 85 90 95  
 Ala Lys Asp Asn Tyr Asp Phe Trp Ser Gly Thr Phe Asp Tyr Trp Gly  
 100 105 110  
 Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 10  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<400> 10  
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30  
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Lys

<210> 11  
<211> 132  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> SIGNAL  
<222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 11  
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg  
-20 -15 -10 -5  
Glu Thr Asn Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro  
1 5 10  
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser  
15 20 25  
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys  
30 35 40  
Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp  
45 50 55 60  
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe  
65 70 75  
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr  
80 85 90  
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys  
95 100 105  
Val Glu Ile Lys  
110

<210> 12  
<211> 138  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Humanized 3D6 light chain variable region

<221> SIGNAL  
<222> (1)...(19)

<400> 12  
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly  
-15 -10 -5  
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln  
1 5 10  
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
15 20 25

Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 30 35 40 45  
 Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser  
 50 55 60  
 Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn  
 65 70 75  
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
 80 85 90  
 Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp  
 95 100 105  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 110 115

<210> 13  
 <211> 393  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(393)  
  
 <221> sig\_peptide  
 <222> (1)...(57)

<400> 13 48  
 atg aag ttg cct gtt agg ctg ttg gta ctg atg ttc tgg att cct gct  
 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala  
 -15 -10 -5  
  
 tcc agc agt gat gtt ttg atg acc caa act cca ctc tcc ctg cct gtc 96  
 Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val  
 1 5 10  
  
 agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag aac att 144  
 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile  
 15 20 25  
  
 ata cat agt aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca 192  
 Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro  
 30 35 40 45  
  
 ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct 240  
 Gly Gln Ser Pro Lys Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser  
 50 55 60  
  
 ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca 288  
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
 65 70 75  
  
 ctc aag atc aag aaa gtg gag gct gag gat ctg gga att tat tac tgc 336  
 Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys  
 80 85 90

ttt caa ggt tca cat gtt ccg ctc acg ttc ggt gct ggg acc aag ctg 384  
 Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu  
 95 100 105

gag ctg gaa 393  
 Glu Leu Glu  
 110

<210> 14  
 <211> 131  
 <212> PRT  
 <213> Mus musculus

<220>  
 <221> SIGNAL  
 <222> (1)...(19)

<400> 14  
 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala  
 -15 -10 -5  
 Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val  
 1 5 10  
 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile  
 15 20 25  
 Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro  
 30 35 40 45  
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser  
 50 55 60  
 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr  
 65 70 75  
 Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys  
 80 85 90  
 Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu  
 95 100 105  
 Glu Leu Glu  
 110

<210> 15  
 <211> 426  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(426)

<221> sig\_peptide  
 <222> (1)...(57)

<400> 15 48  
 atg gac agg ctt act tcc tca ttc ctg ctg att gtc cct gca tat  
 Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr  
 -15 -10 -5

gtc ctg tcc cag gct act ctg aaa gag tct ggc cct gga ata ttg cag	96
Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln	
1 5 10	
tcc tcc cag acc ctc agt ctg act tgt tct ttc tct ggg ttt tca ctg	144
Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu	
15 20 25	
agc act tct ggt atg gga gtg agc tgg att cgt cag cct tca gga aag	192
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys	
30 35 40 45	
ggt ctg gag tgg ctg gca cac att tac tgg gat gat gac aag cgc tat	240
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr	
50 55 60	
aac cca tcc ctg aag agc cgg ctc aca atc tcc aag gat acc tcc aga	288
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg	
65 70 75	
aag cag gta ttc ctc aag acc agt gtg gac cct gca gat act gcc	336
Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala	
80 85 90	
aca tac tac tgt gtt cga agg ccc att act ccg gta cta gtc gat gct	384
Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala	
95 100 105	
atg gac tac tgg ggt caa gga acc tca gtc acc gtc tcc tca	426
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser	
110 115 120	
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<210> 16	
<211> 142	
<212> PRT	
<213> Mus musculus	
<220>	
<221> SIGNAL	
<222> (1)...(19)	
<400> 16	
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-15 -10 -5	
Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln	
1 5 10	
Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu	
15 20 25	
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys	
30 35 40 45	
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr	
50 55 60	
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg	
65 70 75	
Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala	

80 85 90  
Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala  
95 100 105  
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
110 115 120

<210> 17  
<211> 136  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 17  
tccgcgaagct tgccgccacc atggacatgc gcggtgcccgc ccagctgctg ggcctgctga 60  
tgctgtgggt gtccggctcc tccggctacg tgggtatgac ccagtcggcc ctgtccctgc 120  
ccgtgacccc cggcga 136

<210> 18  
<211> 131  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 18  
ctggggggac tggccgggct tctgcagcag ccagttcagg taggtcttgc cgtcggagtc 60  
cagcaggac tggaggact tgcaggagat ggaggcggc tcgccccggg tcacggcag 120  
ggacaggggg g 131

<210> 19  
<211> 146  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 19  
acctgaactg gctgctgcag aagccggcc agtccccca ggcgcgtatc tacctgggt 60  
ccaaagcttga ctccggcgtg cccgaccgct tctccggctc cggctccggc accgacttca 120  
ccctgaagat ctcccgcggt gaggcc 146

<210> 20  
<211> 142  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 20  
aattcttagga tccactcacg cttgatctcc accttgggtgc cctggccgaa ggtgcggggg 60  
aagtgggtgc cctgccagca gtagtacacg cccacgtcct cggcctccac gcgggagatc 120  
ttcagggtga agtcgggtgcc gg 142

<210> 21  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 21  
ctggggggac tggccg 16

<210> 22  
<211> 22  
<212> DNA  
<<213> Artificial Sequence

<220>  
<223> Primer

<400> 22  
acctgaactg gctgctgcag aa 22

<210> 23  
<211> 138  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 23  
acagaaaagct tgccgccacc atggagtttgggctgagctg gctttttctt gtggctat 60  
taaaaagggtgt ccagtgtgag gtgcagctgc tggagtccgg cggcggcctg gtgcagcccg 120  
gcggctccct gcgcctgt 138

<210> 24  
<211> 135  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 24  
gccggccggag cggatggagg ccacccactc caggcccttg ccgggggcct ggcgcaccca 60  
ggacatgccc tagttggaga aggtgaagcc ggaggcggcg caggacaggc gcagggagcc 120  
gccgggctgc accag 135

<210> 25  
<211> 142  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 25  
ctggagtgaaa tggcctccat ccgctccggc ggcggccgca cctactactc cgacaacgtg 60  
aaggccgct tcaccatctc ccgcgacaac gccaagaact ccctgtacct gcagatgaac 120  
tccctgcgcg cccgaggacac cg 142

<210> 26  
<211> 144  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 26  
ctgcaggat ccactcaccc gaggacacgg tcaccagggt gcccggccc cagtagtcgg 60  
aggagccgga gtagtggtcg tagcgcacgc agtagtacag ggcgggtgtcc tcggcgccgca 120  
gggagttcat ctgcaggtac aggg 144

<210> 27  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 27  
gccggccggag cggatg 16

<210> 28  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 28  
ctggagtgaaa tggcctccat 20

<210> 29  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 29  
tccgcaagct tgccgcccc 19

<210> 30  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 30  
aattcttagga tccactcacg cttgatctc

29

<210> 31  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 31  
acagaaaagct tgccgcccacc atg

23

<210> 32  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 32  
ctgcaaggat ccactcacccg ga

22

<210> 33  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> internal peptide

<400> 33  
Asp Ala Glu Phe Arg His Asp Ser Gly Tyr  
1 5 10

<210> 34  
<211> 402  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> h3D6 version 1 VL

<400> 34  
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tccggctacg tggatgac ccagtcggcc 120  
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cagatgaact ccctgcgcgc cgaggacacc gcccgtact actgcgtgcg ctacgaccac 360  
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 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
 35 40 45  
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
 50 55 60  
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
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 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
 85 90 95  
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
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 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
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 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
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 165 170 175  
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
 180 185 190  
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Asp Asp Ser Asp Val  
 195 200 205  
 Trp Trp Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
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 260 265 270  
 Ala Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Val Arg  
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 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
 290 295 300  
 Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
 305 310 315 320  
 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
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 Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr  
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 Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala  
 355 360 365  
 Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp  
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 Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Ala  
 405 410 415  
 Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile  
 420 425 430  
 Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn  
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 Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met  
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 Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys  
 485 490 495  
 Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe  
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 Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser  
 515 520 525  
 Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser  
 530 535 540  
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 580 585 590  
 Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro  
 595 600 605  
 Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
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 Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
 625 630 635 640  
 Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
 645 650 655  
 Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
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 Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
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 Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
 690 695 700  
 Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
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 Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
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